

**Table S2.**

Number of genes that show both age-correlated and disease-correlated gene expression ( $p < 0.001$ ) in the matched regions. Age correlated genes in each region are selected using p cutoff at 0.005. The gene overlapping is done using EntrezID converted based on each microarray platform. Universe is the union of all the genes on training data set (D1 or D2) and target data set (D4 or D5).

Disease dataset	AD (D5)		FTLD-TDP GRN+ (D4)	FTLD-TDP GRN- (D4)
Normal brain aging data set	BA9 (D2)	BA10 (D1)	BA10 (D1)	BA10 (D1)
Number of genes in both datasets	20271	20338	13197	
Number of age- correlated genes	202	72	72	
Number of differentially expressed genes in the disease	735		746	182
Overlap	48	30	54	21
P-value (Fisher's exact test)	0.002	$3.34 \times 10^{-4}$	$2.02 \times 10^{-6}$	$1.21 \times 10^{-4}$